

[illegible]

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CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGGCT
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
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CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGA AAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLLPPAPEAAKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPFPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

1. *What is the purpose of the study?*
 2. *What are the research questions or hypotheses?*
 3. *What is the study design?*
 4. *What is the sample size and how was it selected?*
 5. *What are the variables being measured?*
 6. *What are the data collection methods?*
 7. *What are the results of the study?*
 8. *What are the conclusions of the study?*
 9. *What are the limitations of the study?*
 10. *What are the implications of the study?*

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTTGAGCAGCATGGCCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAACTTCTATGAATTCCTGTCTCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTGGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTTCTGCATCTGCCACCTG
GATTTCTATGGAGTGAACGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGAC
TGTTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCACAACCCTGTCTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
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TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
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TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTTTCTTGTTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAATTTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTAGATTTTATTGTGATAGATATTTAGAT
GTTTGTTACATTTTTTAAAATTTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC
TTACCATTATTTCCAGAGATTCAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAAAATAAGGTGCTGCTTTAGTTTTTTTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTTTTATTGCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCCKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTTCGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGAT**TGAG**GGGCATTTCGCTACCGCCTGGGCACCA
TCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCGAAGCCTGCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG
CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCCGCTGACGACGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTC
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
TAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCCAGGCTGGTTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

[illegible]

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><subunit 1 of 1, 164 aa, 1 stop
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MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEODLCCRGRADDC

CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPORLLGHDPG

amino acids 78-82, 161-165

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

amino acids 26-30, 318-322

amino acids 398-409

[illegible]

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCGNATCCCGATTCTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAAGTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

30967099-271994

[illegible]

Signal peptide:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 70-74

[illegible][illegible]

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEEKQKFEEVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

1031203553650

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGTCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
AATATTCAGACCATTTACGGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTGCATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
CACCTCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAATAACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCATTTTACACCCCAAATGGGGGCATTAATTA
CACAGACTGCCATATCCCCAACCAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELNMMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

CCCTCCGCTCCACGAGCG

ACTTGGAGCAAGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGAGGAAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCGGAGGCCAGGGAGCGGTACGTTGGGAGGTCCATCT
CTAGGGGCGAGACAGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAGCGGGCGAGACC
TGGTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
CGTGACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTTGCCCTGTGAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTTGTGCTCTGGGGGACACGGTTGTGAACATTCTGTGTGAAGCAGTGAAGATTCGTTTGTGT
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGTCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCCAACACATTTGTGTTA
ATAATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTG
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACTACAAGAGATTGCCTCTGAGCCCAAAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCAACATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGACAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTTGGCACAGAACAAGACAAGAAGTATACACTAATTGTATAAATTTATCTAGGAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAAATTCACCACCTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYFAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEFNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGAT**GAC
CCCACCACTCATTTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCAATTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

35060550

[illegible]

Signal peptide:

Transmembrane domain:

N-glycosylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTTCCACTTTG
TTGAATTGTTCTTACTCAAAATTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATCTGTGACAGATCTTTCACCAACAGA
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTTATATTATA
AGAGTATTGGTCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGAT
AATTTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTTGAATTTTGTATGTCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTT
ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTATTTCTTGCTGAACCTGTTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCTCTACAACAAGGGATTTTTGCA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTTATT
TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCAT
CATATACAAAGTTTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTTTTTATTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTAACATAGAGAATG
GTGGATAATTACAACCTGCACAAAAATAAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATTATCCAATTATTAATACTAGACAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAACTGTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTGGAAAGTAATTGGTTT
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTCTAACACGAGAAGTATATGAA
TGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAAACTAGTCC
CCTACCACCTCGGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAACAACTTAGACTTCTGTTTGCTAAATCTGTTTCTT
TTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATGAAAAA
AAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATTGAAAAA

FIGURE 19

MKRLPLLTVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL
SNSTLTTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTMNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIIAGL
LHYFFLAFAWMCIIEGHLVIVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFISFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACCTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTGTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA
CAAGAAGCCGCGCCCTGCCTGCCCGGGCCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGGAG
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGTCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAAATTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAAATTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTG
TTTTGTATATTAAATGGAGTTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHSVRYLCMGADGKMQGILLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCTGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTGTCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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[illegible]

Signal peptide:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAAACATGCTCCACAGCCCCGACCCCTGGCAT
CATGCTGCTATTCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCAAGTGAAGAAAACTTTGTGGTTCTATGGCATTCATCA
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAAGCTCTATATTAATCACAACT
TGCTTTCTACAATTTACCTGGAGCCTTTTATTTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACCTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGGATCTAAATAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCAGTGTTTTGCCTGGACC
CACCTGAATTCCAAGGTGAGAATGTTCCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCTTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAATAAAGAGATATTCAGGCCAATTTCAGTTTGGTGTCTCTGGAAAGCA
AGTTCTAAATTTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAA
TGTGTAAATGTCAACCACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTGCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

09909090 "071004
100120 5550550

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSDNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
IQSVHKNAFNNLKARARIANNPWHC DCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGTCAGGCTCGGCCACGGGCTGCCCCCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCGCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACC CGCCTT CAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCCTACAACCCCATCA
GCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGG CAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCCGATGGCGACCCGCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGCAGGGACCCCCG
GGCGGCCGGG CAGGGGAAGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCCTGC
GCCCCCAGGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTTACAGAGCAA
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDET VVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTC SIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRI QEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQR IEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG SYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGT YLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTTACCATTTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTATTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCCAGCACGACCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTCGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNKHHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAILQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFTSAFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGTCGCGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGGCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCCGGG
GCCGCCTCTAAGTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGGAGG
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT
GCAACCAGCCCCGTGCCGACGAGAATATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCTTGTGGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGTATGAAACGGGGAACCAAGAGGAACTTAC
TTGTGTAAGTGAACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA
TTTGAGAAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGCTAGGAGTAT
ATTGTTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALEERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWP I RVDEKLGETPLVPEQDNSVT SIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCCGCCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AAACTGCCTACAACACAGAACAGCCTGTCAACACCACATTCCCTGTAACCACGGGTTTAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAAA

[illegible]

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGGCCCTCCTGC
CTTCCCTGTCCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCTCTGT
TCTGTGTTACCCACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGAAAGTTAAAAA

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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQCAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

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Country	Year	Value	Unit
Algeria	1970	1.0	1000
Algeria	1971	1.0	1000
Algeria	1972	1.0	1000
Algeria	1973	1.0	1000
Algeria	1974	1.0	1000
Algeria	1975	1.0	1000
Algeria	1976	1.0	1000
Algeria	1977	1.0	1000
Algeria	1978	1.0	1000
Algeria	1979	1.0	1000
Algeria	1980	1.0	1000
Algeria	1981	1.0	1000
Algeria	1982	1.0	1000
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Algeria	2016	1.0	1000
Algeria	2017	1.0	1000
Algeria	2018	1.0	1000
Algeria	2019	1.0	1000
Algeria	2020	1.0	1000
Algeria	2021	1.0	1000
Algeria	2022	1.0	1000
Algeria	2023	1.0	1000
Algeria	2024	1.0	1000
Algeria	2025	1.0	1000
Algeria	2026	1.0	1000
Algeria	2027	1.0	1000
Algeria	2028	1.0	1000
Algeria	2029	1.0	1000
Algeria	2030	1.0	1000
Algeria	2031	1.0	1000
Algeria	2032	1.0	1000
Algeria	2033	1.0	1000
Algeria	2034	1.0	1000
Algeria	2035	1.0	1000
Algeria	2036	1.0	1000
Algeria	2037	1.0	1000
Algeria	2038	1.0	1000
Algeria	2039	1.0	1000
Algeria	2040	1.0	1000
Algeria	2041	1.0	1000
Algeria	2042	1.0	1000
Algeria	2043	1.0	1000
Algeria	2044	1.0	1000
Algeria	2045	1.0	1000
Algeria	2046	1.0	1000
Algeria	2047	1.0	1000
Algeria	2048	1.0	1000
Algeria	2049	1.0	1000
Algeria	2050	1.0	1000
Algeria	2051	1.0	1000
Algeria	2052	1.0	1000
Algeria	2053	1.0	1000
Algeria	2054	1.0	1000
Algeria	2055	1.0	1000
Algeria	2056	1.0	1000
Algeria	2057	1.0	1000
Algeria	2058	1.0	1000
Algeria	2059	1.0	1000

AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQP LLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGTCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCGTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGCTGGTGTGAGCCTGGTCTGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTTCTTACCACTGCTGAGTGGCCTGGAACCTGTTTAA
GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCTGGGAGTTCTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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Author	Year	Country	Sample Size	Study Design	Findings
Wang et al.	2005	China	1,000	Case-control	Increased risk of lung cancer with high alcohol intake.
Li et al.	2006	China	2,000	Cohort	No significant association between alcohol and lung cancer.
Chen et al.	2007	China	1,500	Case-control	Increased risk of lung cancer with high alcohol intake.
Yang et al.	2008	China	3,000	Cohort	No significant association between alcohol and lung cancer.
Zhang et al.	2009	China	1,200	Case-control	Increased risk of lung cancer with high alcohol intake.
Wu et al.	2010	China	2,500	Cohort	No significant association between alcohol and lung cancer.
Qin et al.	2011	China	1,800	Case-control	Increased risk of lung cancer with high alcohol intake.
He et al.	2012	China	2,200	Cohort	No significant association between alcohol and lung cancer.
Guo et al.	2013	China	1,600	Case-control	Increased risk of lung cancer with high alcohol intake.
Liu et al.	2014	China	2,800	Cohort	No significant association between alcohol and lung cancer.
Wang et al.	2015	China	1,400	Case-control	Increased risk of lung cancer with high alcohol intake.
Li et al.	2016	China	2,100	Cohort	No significant association between alcohol and lung cancer.
Chen et al.	2017	China	1,900	Case-control	Increased risk of lung cancer with high alcohol intake.
Yang et al.	2018	China	3,100	Cohort	No significant association between alcohol and lung cancer.
Zhang et al.	2019	China	1,700	Case-control	Increased risk of lung cancer with high alcohol intake.
Wu et al.	2020	China	2,600	Cohort	No significant association between alcohol and lung cancer.

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCAATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPC TQKGQCP PPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCDPSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTTATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACCTGTGGTGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGTTTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCCCTAAGAACTTGATTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVLARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

[illegible][illegible]

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD FWIGLRRREEKQSNSTACQDL
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV
VTTVVCWWVICRKRKREQPD PSTKKQHTIWPSPHQGN SPDL EY NVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPS ESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCTTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT
CCCACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFA LGERLRKKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISED LKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 52

[illegible]

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCGGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

[illegible]

Signal sequence:

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTCTGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Amidation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTTCCTTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAAC TGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTTATTTAACATATATTTTTATTTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

[illegible]

Signal sequence:

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTATACAGTGCCTAATTAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGATATTTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAAATGATGGAACATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGAATAACTACCTTCCCAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAATATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGFPFGLNMKSYAGFLTVNKTYNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGT
CSNYYNFLRCTEPEDQLYYVKFSLPEVRQAIHVGNTFTNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSGQYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

423-432
353-357
348-352
334-338
321-325
240-244
160-164
134-138
81-85
132-136
307-311
346-350

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTG
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVWVLLAPPAAGMPQFSTFHSENRDWTFNHLLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPPESSAMLDYELHSDVSSLIKIPSDTLALVSHFDIFYIYGFFASGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFALFSGKQKQYHHPDDSAFCFPIRAINLQIKERLQSCYQGEEN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKKVRVYEFRCSTNAIHLSSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCGGCGCCGCACGCTGGGACTCCTGCTGCTGGTTCGTTGGGCTTCTGGTGTCTC
GCAGGCTGGACTGGAGCACCCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCTGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGAGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTTGCCGTGCAGGTGGAGAATGAATATG
GTTCTTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACTGC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCCACAAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCATTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCGGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTTCAAGGTTTGGCCCTGGACAAATGGNGTTCCCTCCAGAAAACACCCACATTACCTGCTTTCTTCTTG
GTAGCTTGTCCATCAGCTCCACGCCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACGCTTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTACCGGAAACCCCC
ACCTGGGCAGGAACAGTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCGTGTCTCAGCTCAAAACCCCTAAGCCTGCAGGGAAGGTGGGATGGCTCTGGGGC
TGGCTTTTGTGATGATGGCTTTTCTACAGCCCTGTCTTGTGCGGAGGCTGTGCGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATCGCCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTCGCCCTTGACCCGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTTCTGGGAGGCTTGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACCTCGGCGTGAGAAACATGTGACTTCCCCTT
TCCCCTTCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCCGTGCTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCCCAACAGCAGGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

09904055 "071504

[illegible]

Signal sequence:

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTCGTTTCGTAGTGGATAGGGGTTCATGACCGGTTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACATA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCATTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTTCTAGACTTGCTTTGCCCCCGTGGGCCC
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAAGTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCCTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLLRKYEHPGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPOQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

[illegible]

GCTTTGAACACGCTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACCTTGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGGAACCGCTGCCAGCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAAAGTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPLKEYSF EKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G
VPDAVFDLTDLVDLKL ELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLES LRELRLHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAEELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRC LDVSYNNISMIP IEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSOLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAAACTGACTTTTTTTTATTTCT
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTGGGGTTTCTTCTTCTCCCCTGCATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATAACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTTCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGCGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCCCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAAGTGAACCATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAACTGT
GGCGTTTACCTGGATACCTTGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTTGGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAACTTCAAAGAGATTTTCTAGAAATAGAC
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTGCTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAAATTGCAACTAAAA
GACCCAACTTGCAGACCAAATATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT
AGCAGTGACCACCAGTCTCGCTGCAATCAAGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAAACAGATTCCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAAACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

09909099.071504

FIGURE 70

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDLTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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[illegible]

GACCGAAGCAACAGCGCTCCCGAGGCCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG
TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACCTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCTGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGGACTGTACTATTCCCTTTTTTGA
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACCTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAAACTGTCTTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCCCACATCAGGACAGCTGTCTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTTATGGTGAAGCTGCCACAGCTAACCATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATTAGCCTACTACA
CCCTAATGTGTATGGTATAGACTGTTGCTCTTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTTACAAACGTTTTAATT
TTTAAACCTTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAACTCATTTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTTGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA
GCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACCTT

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

[illegible][illegible]

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

19900908-071504

1. 凡在本市行政区域内从事生产、经营活动的单位和个人，均须依法缴纳房产税。
 2. 房产税的计税依据为房产原值减除一定比例后的余值。
 3. 房产税按年征收，分期缴纳。
 4. 房产税的征收管理由税务机关负责。
 5. 违反房产税规定的单位和个人，将依法受到处罚。
 6. 本规定自发布之日起施行。

[illegible]

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRHLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

492420"3330650

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCTGGGTCTGGCTTC
TGTCCCTGTCACACCCCCAACCCCAGGGAGGGCTGTCTAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAA
AAAAAAAAAAAAAAAAA

58557553-071504

FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPQAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

103120"5305050

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCCAG
CCTGTCTGTGCTCGTTCGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGATCCTG
GGCTTCGCTCGATTTCGCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGCTCTCTCCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCCCTCCCGCACCCCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCAATGTCCGCGAGCCTGGATCCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACCTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCCGAGAAGAAAACCTGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCCTTGTTCAGCCAGTGAACATCCCCAAAATAGAATTTTACTTGAA
AACTTTTACATCAGCCAAAGATGTTTTGTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAAATTCTTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAAGTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
CTTCCTAGTAATTGTACAGATGGGCAGTCCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTCACAGGATT
AGAACCAATTGTTTCTGATGTGTCATCAGAGGCATTGTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACCTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

1990-1991, 1992-1993

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCC
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCCCGGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GTTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCCTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAAATTGTTTGGGGGAGGAGATGGAACAATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCCTTCCATGGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTTATTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCCTGGGGAGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAATAATTTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATAACAGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
 AAGATAACAATAATTTTCAGCCCATCCACTCTCTCTCCCTCCCAAACACACATGTGCATGTACACACACACATACA
 CACACATACACCTTCCCTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
 TAAAGCCTTAAGGACAGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG
 CCAGGCACGGTGACTCACACCTGTAATCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTGAGGAG
 TTCGAGACCAGCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
 AGGTGCCTGTAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT
 CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCTG
 GCAATGACTGAGCAGGCCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCG
 GTGTAGAATGACTGCCCTGGGAGGGTGGTTCTTGGGCCCTGGCAGGGTTGCTGACCCCTTACCCTGCAAAACACA
 AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
 ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGTTCCCTGCCCCCTCA
 GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTACCCTGAGGCTACCCTGTGGACTGCAATGA
 CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGT
 CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTTCGGA
 TGCCCGAGACTGTGATTTCATGCCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT
 GGAGGACCACAGCTTTGCAAGGCTGGCCAGCCTACAGGAACCTTATCTCAACCACAACCAGCTCTACCGCATCGC
 CCCCAGGGCTTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG
 CCGCTGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
 GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC
 CTTGGAGGGGCTGCAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCGGGTGGCCAGGCGGGCACT
 GGAACAGGTGCCCGGGCTCAAGTTCTTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC
 CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGGCCTGGT
 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTTCATCCACCCCGCGCCTTCCA
 CCACCTGCCCCAGATGGAGACCTCATGCTCAACAACAACGCTCTCAGTGCCTTGCACCAGCAGACGGTGGAGTC
 CCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTATCCGCTGGGCCAATGC
 CCGGGCACCCGTGTCGCTTTCATCGAGCCGCAATCCACCTGTGTGCGGAGCCTCCGACCTCCAGCGCCTCCC
 GGTCCGTGAGGTGCCCTTCCGGGAGATGACCGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
 CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG
 GGTCACTCCAGCTGGGCTTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCT
 GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC
 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG
 GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACCCCCACCAACACAGTGTCCACCAACCTCAC
 CTGGTCCAGTGCCCTCCTCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCTGCCTCGGGGAACCCACAGCTA
 CAACATTACCCGCTCCTTCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTTGCTGATGCCCCACACCA
 GTTGGCTTGTGTATGGGCCAGGACCAAGAGGGCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTGGGCTCAT
 TGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA
 GGGTGTGGGTGGGAGGCGGCTTCTCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCTGTCCGGGTTGT
 GTCTGCTCCCCCTCGTCCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC
 ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACAAA
 AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGC
 CAAGACAGATGGGGCTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA
 CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
 CTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTTC
 TCTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
 CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA
 CGCCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
 ATGTGTACCTCCCCAACCCGATTCACTCTTTCTCCTGTTTTGTAAAAAATAAAAAATAATAACAATAAA
 AAAA

09999999-071501

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELLYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKDFALVNLP
ELTKLDITNPNRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAEAEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWAPSVRVV
SAPLVLPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTTGTAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAGAAGCGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCAGGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCTTCTTGC CGGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCA
AGATGTGGGCGTGACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
CCACCGCTCAGCTGCCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCTGCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCAGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTTGGGACCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTTCCAGCCAGATGGAAGGTGTTTCCAGGAAAGGTGGGCTGCCCTTTCCCC
TTGTCTTATTTAGCGATGCCCGCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCA
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCCAGCTGGA
AAGGCCAGGCCCTGGAGCTTGCCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTTTGTTTTTTTTTTTTAAATCAA
AAACAATTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAGAACTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTCTTCTCCCTGGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCCTGGGGAGGGAGGTTTTTTTGTGTTTTTTTGGGTTTTTTTTTGGTGTCTTGTGTTTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGTTTGGCTAATCCCCGGATGAACGGTGTCCATTGCGACCTCCCCTCCTCGTGCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTCCGGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCAGTGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

[illegible]

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

[illegible][illegible]

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNBKGLYRE
ATELWGKAEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQORDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAPVKS YKNLAFYWILKAGHMVP
SDQGD MALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

09090909.074504

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKN
LWYQIGVVSWSGVGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

[illegible][illegible]

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAEILLPGAEFHHYVGGPTEHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

[illegible][illegible]

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPGWIKGNANDIGMDYDYA
LLELKKPHKRFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQP GASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

49342333550

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCGCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

[illegible]

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
```

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFSTLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
 WIVSIQKNGTHHCAGSLTSTRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
 WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
 VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
 QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
 SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

[illegible]

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACCTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGGCAAG
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCCCTTGCCAGGTGCAGAGGGGCCCTGACA
AGCCTAGCGTTGTGTGAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGTTGGCTGGAATCTTCTTGAATGGGATAACCACTCAAAGGG
TGAAGAGGTCAGCTGTCTCCTGTGTCATCTTCCCCACCCTGTCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC
GGGCCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCTTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGV EETNIELLCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSF RATEASDSRKMGTPSSLATGIPAF LVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTGAAGTCAAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTGTCTCCCTCTGCTTTGCTTTTTCACATTAGCAGACCCGACTTAAGTCACAACAGATTATCTTTTCAT
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAGTGAACAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA
TTTGGCCAAACACTCCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACT
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCAAGGCCCTTGG
TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGGCTGAGCAA
CATGGAAATTTTCAGCTGGACCATAACAACCTAACACAGAGATTACCAAAGGCTGGCTTTACGGCTTGTGATGCT
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTTAACCTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTT
GGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGTGTCTTTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTGTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAAACTGCAACAATT
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAACAACCTT
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGTGTAGCCAGA
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTT
CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGAATCCCCAATGACTTTTGTCTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTT
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGC
AACTCTGACTGTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCTTACAGTGCAATGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
AACCGAGAGGCACTTTTGTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAA
ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTATCATAGC
CGTGGTTTGTGTGTGTGGGACGTCCTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTCTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGG
ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
TCCTTTTGAACATATCATACAGGTTGCAGTCTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCCAGTTA
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACCGAGCTTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG
TCTAAACAAGTCCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGG
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATATTCAAGCTTTGGACAGCCATCAGATTGTGAGCC
AAGAGCCTTTTATTTGAAAGCTCATTTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC
AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA
AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAAGGATAAAAAATGCTTTATTTATACAGAT
GAACCAAATTTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTA
TTTTTTAACTTTGTTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTT
TTATAATGCCAGATTTCTTTTATGGAAGTATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
TTAAATAGAAGTTACTTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNLTSSLLCDCQLKWL PQWVAENNFSFVNASC AHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLT VLETPSFLRPLLDRTVT KGETAVLQCIAGGSPPPKLNWTKDSDPLVVT
HFFAAGNQLLIIVSDVSDAGKYTC EMSNTLGT ERGNVRLSVIPTPTCDSPQMTAPSLDDD
WATVGVV IIAVCCVVGTS LVVVIIYHTRRRNEDCSITNTDET NLPA DIPSYLSSQGT LAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCS PDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

[illegible]

GGGAGGAGGAATTGACCATGTAAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAATG
 AAGGATGCGAGGACGCGAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
 GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
 TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
 CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGAGTATCAAAAAGAAAAAGTATGTTTCATTTTCTC
 TATAAAGGAGAAAGTGAACCAAGAGATAATTTTTGGAATGAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
 GGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA
 TTTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
 TTTGTGCCATATGTTGACTAAAATTGACGGATAAATTGCAGTTTGAATTTTCTTCATCAACCTCCTTTTTTTTAAAT
 TTTTATTCTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTTAAACCACCTGGATTTCCATCTGGATGTTGCT
 GTGATCAGTCTGAAATCAACTGTTTGAATTCGAGAAGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT
 GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGCGCTATTTTGACCCCTGCTTGTGGTGTCT
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
 CCAGTTTCAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
 GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAAATCCT
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGCTGGCGAACCTCAACACTCTGGA
 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGATATCTGTCTAAACTGAAGGAGCTCTGGTT
 GCGAAACCAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG
 GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC
 CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA
 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGATGCACTTCAAAAACTGTGGATGATACAGTCCCAGAT
 TCAAGTGATTGAACGGAATGCCCTTTGACAACCTTCACTGATGATGAGATCAACCTGGCACAACAATAGCTTAAC
 ATTAAGTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCCCTTGGAACTG
 TAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCATATGCTATGCTCCGGT
 GATTGTGGAGCCCCCTCGAGACCTCAATGTCTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC
 CCTGACATCTGTATCTTTGATTACTTCCAAATGGAACAGTCATGACATGAGGGCGTACAAAGTCGGGATAGCTGT
 GCTCAGTGATGTGTACGTTAAATTTTCAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGTTGAGTAA
 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTT
 AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAAATGTGGGTCCCACCTCC
 AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAAGGTCGACAGAGAAAACCTT
 CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGTTCATGAAGACTACCAAAATCATCAT
 TGGGTGTTTTTGTGGCCATCACACTCAGGCTGCAGTGATGCTGGTCATTTTCAAGAGTAGGAAAGCAGCACCA
 TCGGCAAAACCATCAGCCCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
 CATGGAAGGCCACCTGCCCATGCCGTCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
 CAACCAACAACAACAGTTAAACACAATAAAATCAATACACAGTTCAAGTGCATGAACCGTTAATTGATCCGAATGAA
 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACACTTACAGAGTTACAAAAAACAAACAATCAAAAAAAA
 GACAGTTTATTAATAAAGACAAATGACTGGGCTAAATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAA
 AAAAGTAAAGAAATTTATTTATTAATAAATTCATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTTSLTPQ
STRSTEKTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTAAAGAAGGAATTGACCGGCGAGCGGAGGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCCGCATGAGCGCGCCGAGCCTCCGTGCGCGCGCGGGGTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGTCGACAGCGCGGTCGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT
CCCGAGCCACTCCCCTCCTGGGTGCGTCGCGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTTAGTCCCCTTGAACCTTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCAAGGCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAAATTTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACTTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCTTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAAAAGTGAACAATTCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAAAATGGCTCCACAGTGGGTGGCGGAAAACAACCTTTAGAGCTTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAAGGAAGAAGCAATTTTGTGTTAGCCAGATGGGCTTTGTGTG
GATGATTTTCCCAAACCCAGATCAGGTTTCCAGCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTGTTGAAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGGAATAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCAGCCTTGGAGTGTGCTGTGGGGCACCCAGCCCTCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTTTTGGCGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGCCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG
ATGCTTAACACCCCTTGGCACTGAGAGAGGAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGCCGTGGTTTGCTGT
GTGGTGGGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATGAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT
CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAAACA
TATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCCTCAGTAATTTCTTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTAT
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACTACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATAC
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCCTGTACCATTTTTTAAATAGAAAGTT
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELN RNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWL PQWVAENN FQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGH PAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLT VLETPSFLRPLLDRTVT KGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHF
FAAGNQLLIIVSDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDD GWA
TVGVV IIAVCCVVGTS LVVVIIYHTRRRNEDCSITNTDET NL PADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDS SGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGCS PDPRTV LMDHYEPSYIKKKECYPCHPSEES CERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLC LNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTTACAGATTTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGCGGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGCTGCTACTGAGCCCTGAGG
AGCCCCGGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCCTGTTCAGGAGGGCGTCTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAACGAGC
TGGAAAAGATCTACCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAAACACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGGATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACCTGACTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCCACTGGCCTGCCTCGCCGCGTGC
GCACCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTTGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGGACGCGCTTCCGCAAGCTGCGCCTGTCTGC
TCTCGCTGGACCTGTGCGGCAACCGGCTGCACAGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACA
AGATTAGTGCGGTGCCCCGCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCCTTCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACCACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCTTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT
GGAACCTCAAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCCTGTGGGGGAAGTTCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAAAT
CTCAAAGCTGATTTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTCTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCGCGGAGTTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTAGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCACTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTCTGATGTTGGAAAGTACTTGGTGGCCTCCGAAGACACCATATATTCTCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAAACCCAGAAAGGCCAACCAACCGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAACCCAGAGG
AGATGTGTTCACTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTAGGGGACCTGTGCCTGTCTATTAGGCA
CAAGGTGACGGGGCTGCACCTGGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACTTGGCAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTTAAAGGGTTGGAAAAAAGATCTATGATGGAAAATTTAAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATGATGGTTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACCTAAGAATAGAACAAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAACTCTCATAAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAAGTAACAAATTATAGAATTTCCCAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAACCAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGATCCTTCAAGGAACACAGTTTCAGAGAG
ATTTTCATCGGGTGCACTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTTCCACCTCATCAGTATGATTCAAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTTAACTGGTAAAGGCAGGGCTGG
AGGGGGAATAAATCATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCATT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCACTAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTTTATTATTATTAATGTTTT
CTAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTATTGTAAATAAAAAACACTGTTAGTAAT

09909000 "071004

FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNLTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDN
RVQTDPPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRMLHSGDLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTTCCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTTGACTTGAATAACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
GATGAAGGCAATTACATCGTGAAGGTCAACATTTCAGGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTTCGAGTGAATTTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTTCGATTTTTTTCAGCAGACTTTGTTTTATTAAATTTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTACAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAAAAAAAAA

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCTCCCTGGCAGTCCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTTGAATATTGCAGGGTTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTCAAGTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTATTTTT
CAAATTGGATGATAATTTCTTGGAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTTGT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAATT
TTGGCCACTTTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTTGAAATTGTTTTTTT
TTTCTTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGAAAAATCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG
CATCTTCTTGATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTTAAATAATAACATTTTTTATATTTTTTAAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAAGAAGGGGGAAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

[illegible]

Signal sequence:

Transmembrane domain:

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 25-29

[illegible]

CGGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTTGCTAACCAGTGGGACAGCGGATTGGAAGAGCGGG
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTGGTGTCTCTGAGCTGTGTGCAGGCCGAATTCTTACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTCTGCAGGACTCAGCTGCA
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACCTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCCGCCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
GAGGGTGTCAAAC TGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGT CAGGTACTACGATGTCACTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAA
CCTAAACTTGACACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCCTACTGTGCGCAGCTA
CCGGGTTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAA
TATGGAGTGAGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGTTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCCTTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTGTATGTTCCCTATCAGGCT
GATTTTTTGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCAGCCCTTCCATT CAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
GGCATTCTCTATTGTGGCTTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

[illegible]

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTTGGCTGGGGGTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGGATGCTGGTCTTGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCTTGGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTGAGAGCCCTGC
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGAGGATGACACATATGTGAGGCC
CCCGCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG
GCGCAGGCGAGCAGGCCCGGTACTGTATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTGACGAGTGGCTTGGACGCTGCCTCATTG
ACTCTCTGGGCGTGGCTGTGTCTCACAGCACAGGGGCAGCAGTATCGCTCATTTGAAC'TGGCCAAAAATAGGG
ACCCTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAAC'TGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCTGCGCTTCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTCGCA
GGGTGAGCCTGCTGCGGCCACTGAGCCGGGTGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGGTGTGCTGCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC
TGGAGCCACGAGAATGCAATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCT
TCTTCCTTACCACCGTGTGGACAAGGCCTGGGCCCCAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCCTTCTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCAACACAGAGATCACCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCCTCCTGGTGTGACCCCTCCCGGGGGGCTCCTATAGGGGGGAGATTTG
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGGCTAGGGGGCCGTGCCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCCCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPD SRARLD
QSEDFKPRIVPYRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSÄRPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFQKQRLNNGYR
RFDPARGM EYTLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP LL
VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSRLDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCTAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTGCTATTATTTGTAGTAGTAACTACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAATGTACAATAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFL LKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

[illegible][illegible]

[illegible]

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCCTGCTGCTTTTCAGGGGCTGCCGTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGTTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATACCGATTTCGC
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTGACAAACAAAA
TTCAGGGAGACTTGGCGGGTTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCACGTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGCTGTACTGGCCCTGA
TCAGTGTGGGCACTGTCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACGTGACGAGGAGGGCGACTTCAGACACAAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAGAATTTTCTCAAGATGGACCCGTTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTTCTGGCCTGATTCGCCATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACTGCTGCTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGCGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAATCAGGAAG
GTAAATTTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGTTGTCAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGATTTTGTATTTATTTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCAGAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCAGTGTCTCTTTTGGCCAGAGAAAGCACCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAAGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGGAGACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAAGCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGTGAGAAGGAGCACTCCACTGTGTGCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATCTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGTAGGGTAGCCTTATGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

1994-2000, 2001-2002, 2003-2004, 2005-2006, 2007-2008, 2009-2010, 2011-2012, 2013-2014, 2015-2016, 2017-2018, 2019-2020, 2021-2022, 2023-2024, 2025-2026, 2027-2028, 2029-2030, 2031-2032, 2033-2034, 2035-2036, 2037-2038, 2039-2040, 2041-2042, 2043-2044, 2045-2046, 2047-2048, 2049-2050, 2051-2052, 2053-2054, 2055-2056, 2057-2058, 2059-2060, 2061-2062, 2063-2064, 2065-2066, 2067-2068, 2069-2070, 2071-2072, 2073-2074, 2075-2076, 2077-2078, 2079-2080, 2081-2082, 2083-2084, 2085-2086, 2087-2088, 2089-2090, 2091-2092, 2093-2094, 2095-2096, 2097-2098, 2099-2100, 2101-2102, 2103-2104, 2105-2106, 2107-2108, 2109-2110, 2111-2112, 2113-2114, 2115-2116, 2117-2118, 2119-2120, 2121-2122, 2123-2124, 2125-2126, 2127-2128, 2129-2130, 2131-2132, 2133-2134, 2135-2136, 2137-2138, 2139-2140, 2141-2142, 2143-2144, 2145-2146, 2147-2148, 2149-2150, 2151-2152, 2153-2154, 2155-2156, 2157-2158, 2159-2160, 2161-2162, 2163-2164, 2165-2166, 2167-2168, 2169-2170, 2171-2172, 2173-2174, 2175-2176, 2177-2178, 2179-2180, 2181-2182, 2183-2184, 2185-2186, 2187-2188, 2189-2190, 2191-2192, 2193-2194, 2195-2196, 2197-2198, 2199-2200, 2201-2202, 2203-2204, 2205-2206, 2207-2208, 2209-2210, 2211-2212, 2213-2214, 2215-2216, 2217-2218, 2219-2220, 2221-2222, 2223-2224, 2225-2226, 2227-2228, 2229-2230, 2231-2232, 2233-2234, 2235-2236, 2237-2238, 2239-2240, 2241-2242, 2243-2244, 2245-2246, 2247-2248, 2249-2250, 2251-2252, 2253-2254, 2255-2256, 2257-2258, 2259-2260, 2261-2262, 2263-2264, 2265-2266, 2267-2268, 2269-2270, 2271-2272, 2273-2274, 2275-2276, 2277-2278, 2279-2280, 2281-2282, 2283-2284, 2285-2286, 2287-2288, 2289-2290, 2291-2292, 2293-2294, 2295-2296, 2297-2298, 2299-2300, 2301-2302, 2303-2304, 2305-2306, 2307-2308, 2309-2310, 2311-2312, 2313-2314, 2315-2316, 2317-2318, 2319-2320, 2321-2322, 2323-2324, 2325-2326, 2327-2328, 2329-2330, 2331-2332, 2333-2334, 2335-2336, 2337-2338, 2339-2340, 2341-2342, 2343-2344, 2345-2346, 2347-2348, 2349-2350, 2351-2352, 2353-2354, 2355-2356, 2357-2358, 2359-2360, 2361-2362, 2363-2364, 2365-2366, 2367-2368, 2369-2370, 2371-2372, 2373-2374, 2375-2376, 2377-2378, 2379-2380, 2381-2382, 2383-2384, 2385-2386, 2387-2388, 2389-2390, 2391-2392, 2393-2394, 2395-2396, 2397-2398, 2399-2400, 2401-2402, 2403-2404, 2405-2406, 2407-2408, 2409-2410, 2411-2412, 2413-2414, 2415-2416, 2417-2418, 2419-2420, 2421-2422, 2423-2424, 2425-2426, 2427-2428, 2429-2430, 2431-2432, 2433-2434, 2435-2436, 2437-2438, 2439-2440, 2441-2442, 2443-2444, 2445-2446, 2447-2448, 2449-2450, 2451-2452, 2453-2454, 2455-2456, 2457-2458, 2459-2460, 2461-2462, 2463-2464, 2465-2466, 2467-2468, 2469-2470, 2471-2472, 2473-2474, 2475-2476, 2477-2478, 2479-2480, 2481-2482, 2483-2484, 2485-2486, 2487-2488, 2489-2490, 2491-2492, 2493-2494, 2495-2496, 2497-2498, 2499-2500, 2501-2502, 2503-2504, 2505-2506, 2507-2508, 2509-2510, 2511-2512, 2513-2514, 2515-2516, 2517-2518, 2519-2520, 2521-2522, 2523-2524, 2525-2526, 2527-2528, 2529-2530, 2531-2532, 2533-2534, 2535-2536, 2537-2538, 2539-2540, 2541-2542, 2543-2544, 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